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<110>   Allan, Barrett W.
         Davies, Julian
         Marquis, David M.
         Ondek, Brian
         Watkins, Jeffry D.

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His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
        35   40   45

Ala Thr Ser Ala Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50   55   60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
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Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Arg Thr Phe Thr Ser Tyr
            20   25   30

Asn Met His Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45

Gly Ala Ile Tyr Pro Leu Thr Gly Asp Thr Ser Tyr Asn Gln Lys Ser
    50   55   60

Lys Leu Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
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        35   40   45

Ala Thr Ser Gly Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
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Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
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aaagttccta agctcttgat ctatgccaca tccggcctgg cttctggggt cccatctcgg     180

ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagcct gcagcctgaa     240

gatgttgcca cttattactg ccagacttgg acttttaacc ctcccacgtt cggcggaggg     300

accaaggtgg agatcaaa                                                    318


<210>  65
<211>  121
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<220>
<223>  Synthetic construct


<220>
<221>  MISC_FEATURE
<222>  (1)..(121)
<223>  AME 5 HCVR

<400>  65
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
            35   40   45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
        50   55   60

Lys Trp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

```
Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Gln Phe Asp Glu Trp Gly
        100             105             110

Lys Gly Thr Thr Val Thr Val Ser Ser
        115             120
```

<210> 66
<211> 363
<212> DNA
<213> artificial

<220>
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<220>
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<222> (1)..(363)
<223> AME 5 HCVR

<400> 66
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tcctgcaagg catctggata caccttcacc agctacaata tgcactgggt gcgacaggcc     120

cctggacaag ggcttgagtg gatgggagcc atctatcctg gaaatggtga tacaagctac     180

aatcagaagt ttaaatggag agtcaccatg accagggaca cgtccacgag cacagtctac     240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagatcgact     300

tattacggcg gtgactggca gttcgacgag tggggcaaag ggaccacggt caccgtctcc     360

tca                                                                   363
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<210> 67
<211> 213
<212> PRT
<213> artificial

<220>
<223> Synthetic construct

<220>
<221> MISC_FEATURE
<222> (1)..(213)
<223> AME 33 complete light chain

<400> 67

```
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5               10              15


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Pro Tyr Ile
        20              25              30
```

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His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
        35   40   45

Ala Thr Ser Ala Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50   55   60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65   70   75   80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Leu Ser Asn Pro Pro Thr
                85   90   95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
            100   105   110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115   120   125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
            165   170   175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180   185   190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195   200   205

Asn Arg Gly Glu Cys
    210

<210>   68
<211>   642
<212>   DNA
<213>   artificial

<220>
<223>   Synthetic construct

<220>
<221>   misc_feature
<222>   (1)..(642)
<223>   AME 33 complete light chain

<400>   68

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ctctcctgca gggccagctc aagtgtaccg tacatccact ggtaccagca gaaacctggc   120

caggctccca ggctcctcat ctatgccaca tccgctctgg cttctggcat cccagacagg   180

ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagact ggagcctgaa   240

gattttgcag tgtattactg tcagcagtgg ctgagtaacc acccactttt ggccagggg   300

accaagctgg agatcaaacg aactgtggct gcaccatctg tcttcatctt cccgccatct   360

gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc   420

agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag   480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg   540

agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg   600

agctcgcccg tcacaaagag cttcaacagg ggagagtgtt ag                      642
```

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<210>  69
<211>  451
<212>  PRT
<213>  artificial

<220>
<223>  Synthetic construct


<220>
<221>  MISC_FEATURE
<222>  (1)..(451)
<223>  AME 33 complete heavy chain

<400>  69
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```
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5               10              15


Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Arg Thr Phe Thr Ser Tyr
            20              25              30


Asn Met His Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35              40              45


Gly Ala Ile Tyr Pro Leu Thr Gly Asp Thr Ser Tyr Asn Gln Lys Ser
    50              55              60


Lys Leu Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65              70              75              80


Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
            85              90              95


Ala Arg Ser Thr Tyr Val Gly Gly Asp Trp Gln Phe Asp Val Trp Gly
```

```
                                  100                       105                         110


            Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
                    115               120               125


            Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
                130               135               140


            Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
            145               150               155               160


            Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                            165               170               175


            Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
                            180               185               190


            Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
                    195               200               205


            Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
                210               215               220


            Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
            225               230               235               240


            Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                            245               250               255


            Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
                    260               265               270


            Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                    275               280               285


            His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                290               295               300


            Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            305               310               315               320


            Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                            325               330               335


            Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
                        340               345               350


            Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
```

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355   360   365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370   375   380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385   390   395   400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            405   410   415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420   425   430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    435   440   445

Pro Gly Lys
    450

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<220>
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<220>
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<222> (1)..(1356)
<223> AME 33 complete heavy chain

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tcctgtaagg gttctggccg tacatttacc agttacaata tgcactgggt gcgccagatg   120
cccgggaaag gcctggagtg gatggggggct atttatccct tgacgggtga tacttcctac   180
aatcagaagt cgaaactcca ggtcaccatc tcagccgaca agtccatcag caccgcctac   240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagatcgact   300
tacgtgggcg gtgactggca gttcgatgtc tggggcaagg ggaccacggt caccgtctcc   360
tcagcctcca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct   420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg   480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc   540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag   600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaggttgag   660

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cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg    720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc    780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac    840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac    900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc    960

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc   1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggac   1080

gagctgacca gaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac   1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc   1200

gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   1320

acgcagaaga gcctctccct gtctccgggt aaatga                             1356
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<210>  71
<211>  23
<212>  PRT
<213>  Homo sapiens


<220>
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<223>  FRL1 VkIII (A27)(DPK22)

<400>  71

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Ser Cys
            20


<210>  72
<211>  15
<212>  PRT
<213>  Homo sapiens


<220>
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<222>  (1)..(15)
<223>  FRL2 VkIII (A27)(DPK22)

<400>  72

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1               5                   10                  15


<210>  73
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<211>    32
<212>    PRT
<213>    Homo sapiens


<220>
<221>    MISC_FEATURE
<222>    (1)..(32)
<223>    FRL3 VkIII (A27)(DPK22)

<400>    73

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1               5                   10                  15


Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
            20                  25                  30


<210>    74
<211>    10
<212>    PRT
<213>    Homo sapiens


<220>
<221>    MISC_FEATURE
<222>    (1)..(10)
<223>    FRL4 VkIII (A27)(DPK22)

<400>    74

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1               5                   10


<210>    75
<211>    69
<212>    DNA
<213>    Homo sapiens


<220>
<221>    misc_feature
<222>    (1)..(69)
<223>    FRL1 VkIII (A27)(DPK22)

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60

ctctcctgc                                                               69


<210>    76
<211>    45
<212>    DNA
<213>    Homo sapiens


<220>
<221>    misc_feature
<222>    (1)..(45)
<223>    FRL2 VkIII (A27)(DPK22)
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<400> 76
tggtaccagc agaaacctgg ccaggctccc aggctcctca tctat   45

<210> 77
<211> 96
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(96)
<223> FRL3 VkIII (A27)(DPK22)

<400> 77
ggcatcccag acaggttcag tggcagtggg tctgggacag acttcactct caccatcagc   60

agactggagc ctgaagattt tgcagtgtat tactgt   96

<210> 78
<211> 30
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(30)
<223> FRL4 VkIII (A27)(DPK22)

<400> 78
tttggccagg ggaccaagct ggagatcaaa   30

<210> 79
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> FRH1 VH5-51 (DPK-73)

<400> 79

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1   5   10   15

Ser Leu Lys Ile Ser Cys Lys Gly Ser
            20   25

<210> 80
<211> 14
<212> PRT
<213> Homo sapiens

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<220>
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<222>   (1)..(14)
<223>   FRH2 VH5-51 (DP-73)

<400>   80

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
1               5                   10


<210>   81
<211>   32
<212>   PRT
<213>   Homo sapiens


<220>
<221>   MISC_FEATURE
<222>   (1)..(32)
<223>   FRH3 VH5-51 (DP-73)

<400>   81

Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1               5                   10                  15


Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>   82
<211>   11
<212>   PRT
<213>   Homo sapiens


<220>
<221>   MISC_FEATURE
<222>   (1)..(11)
<223>   FRH4 VH5-51 (DP-73)

<400>   82

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
1               5                   10


<210>   83
<211>   75
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(75)
<223>   FRH1 VH5-51 (DP-73)

<400>   83
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tcctgtaagg gttct                                                        75
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<210> 84
<211> 96
<212> DNA
<213> Homo sapiens

<220>
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<223> FRH2 VH5-51 (DP-73)

<400> 84
tgggtgcgcc agatgcccgg gaaaggcctg gagtggatgg ggcaggtcac catctcagcc   60

gacaagtcca tcagcaccgc ctacctgcag tggagc   96

<210> 85
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<213> Homo sapiens

<220>
<221> misc_feature
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<223> FRH3 VH5-51 (DP-73)

<400> 85
agcctgaagg cctcggacac cgccatgtat tactgtgcga ga   42

<210> 86
<211> 33
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(33)
<223> FRH4 VH5-51 (DP-73)

<400> 86
tggggcaagg ggaccacggt caccgtctcc tca   33

<210> 87
<211> 23
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(23)
<223> FRL1 VkI (DPK4)(A20)

<400> 87

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys
            20

<210>   88
<211>   15
<212>   PRT
<213>   Homo sapiens

<220>
<221>   MISC_FEATURE
<222>   (1)..(15)
<223>   FRL2 VkI (DPK4)(A20)

<400>   88

Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr
1   5   10   15

<210>   89
<211>   32
<212>   PRT
<213>   Homo sapiens

<220>
<221>   MISC_FEATURE
<222>   (1)..(32)
<223>   FRL3 VkI (DPK4)(A20)

<400>   89

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys
            20   25   30

<210>   90
<211>   10
<212>   PRT
<213>   Homo sapiens

<220>
<221>   MISC_FEATURE
<222>   (1)..(10)
<223>   FRL4 VkI (DPK4)(A20)

<400>   90

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1   5   10

<210>   91
<211>   69
<212>   DNA

<213> Homo sapiens

<220>
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<223> FRL1 VkI (DPK4)(A20)

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc   60

atcacttgc   69

<210> 92
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<212> DNA
<213> Homo sapiens

<220>
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<223> FRL2 VkI (DPK4)(A20)

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<210> 93
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<212> DNA
<213> Homo sapiens

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<223> FRL3 VkI (DPK4)(A20)

<400> 93
ggggtcccat ctcggttcag tggcagtgga tctgggacag atttcactct caccatcagc   60

agcctgcagc ctgaagatgt tgccacttat tactgc   96

<210> 94
<211> 30
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(30)
<223> FRL4 VkI (DPK4)(A20)

<400> 94
ttcggcggag ggaccaaggt ggagatcaaa   30

<210> 95
<211> 25
<212> PRT

<213>   Homo sapiens

<220>
<221>   MISC_FEATURE
<222>   (1)..(25)
<223>   FRH1 VkI (DP7/21-2)

<400>   95

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser
                20   25

<210>   96
<211>   14
<212>   PRT
<213>   Homo sapiens

<220>
<221>   MISC_FEATURE
<222>   (1)..(14)
<223>   FRH2 VkI (DP7/21-2)

<400>   96

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1   5   10

<210>   97
<211>   32
<212>   PRT
<213>   Homo sapiens

<220>
<221>   MISC_FEATURE
<222>   (1)..(32)
<223>   FRH3 VkI (DP7/21-2)

<400>   97

Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
1   5   10   15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
                20   25   30

<210>   98
<211>   11
<212>   PRT
<213>   Homo sapiens

<220>
<221>   MISC_FEATURE

```
<222>   (1)..(11)
<223>   FRH4 VkI (DP7/21-2)

<400>   98

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
1               5                   10


<210>   99
<211>   75
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(75)
<223>   FRH1 VkI (DP7/21-2)

<400>   99
caggtgcagc tggtgcagtc tggtgctgaa gtgaagaagc ctggggcctc agtgaaggtg     60

tcctgcaagg catct                                                     75


<210>   100
<211>   40
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(40)
<223>   FRH2 VkI (DP7/21-2)

<400>   100
ggtgcgacag gcccctggac aagggcttga gtggatggga                          40


<210>   101
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<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(96)
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agagtcacca tgaccaggga cacgtccacg agcacagtct acatggagct gagcagcctg     60

agatctgagg acacggccgt gtattactgt gcgaga                              96


<210>   102
<211>   33
<212>   DNA
<213>   Homo sapiens
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<222>  (1)..(33)
<223>  FRH4 VkI (DP7/21-2)

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tggggcaaag ggaccacggt caccgtctcc tca                                    33
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